**Figure 1**

MRGPAVLLTV	ALATLLAPGA	GAPVQSQGSQ	NKLLLVSFDG	FRWNYDQDQD
TPNLDAMARD	GVKARYMTPA	FVTMTSPCHF	TLVTGKYIEN	HGVVHNMYYN
TTSKVKLPYH	ATLGIQRWWD	NGSVPIWITA	QRQGLRAGSF	FYPGGNVTYQ
GVAVTRSRKE	GIAHNYKNET	EWRANIDTVM	AWFTEEDLDL	VTLYFGEPDS
TGHRYGPESP	ERREMVRQVD	RTVGYLRESI	ARNHLTDRLN	LIITSDHGMT
TVDKRAGDLV	EFHKFPNFTF	RDIEFELLDY	GPNGMLLPKE	GRLEKVYDAL
KDAHPKLHVY	KKEAFPEAFH	YANNPRVTPL	LMYSDLGYVI	HGRINVQFNN
GEHGFONKDM	DMKTIFRAVG	PSFRAGLEVE	PFESVHVYEL	MCRLLGIVPE
ANDGHLATLL	PMLHTESALP	PDALLVADGP	CLPSLSQAKG	CMPLSPAAPT
PAWLLWCW				

**Figure 2**

3/14

10 20 30 40 50 60 70  
GTCCATCTGGAAGGCCAGCATGAGAGCCCGGCCGTCTCTCACTGTGGCTCTGGCCACGCTCCTGGCTCCCGGGG  
M R G P A V L L T V A L A T L L A P G A  
80 90 100 110 120 130 140 150  
CCGGAGCACCGGTACAAAGTCAGGGCTCCCGAACAAGCTGCTCCTGGTGTCTTCGACGGCTTCCGCTGGAACCTACG  
G A P V Q S Q G S Q N K L L L V S F D G F R W N Y D  
160 170 180 190 200 210 220 230  
ACCAGGACGTGGACACCCCAACCTGGACGCCATGGCCCGAGACGGGGTGAAGGCACGCTACATGACCCCGCCTTTG  
Q D V D T P N L D A M A R D G V K A R Y M T P A F V  
240 250 260 270 280 290 300 310  
TCACCATGACCAGCCCTGCCACTTCACCCTGGTCACCGGCAAATATATCGAGAACCACGGGGTGGTTCAACATGT  
T M T S P C H F T L V T G K Y I E N H G V V H N M Y  
320 330 340 350 360 370 380 390  
ACTACAACACCACCAGCAAGGTGAAGCTGCCCTACCACGCCACGCTGGGCATCCAGAGGTGGTGGACAACGGCAGCG  
Y N T T S K V K L P Y H A T L G I Q R W W D N G S V  
400 410 420 430 440 450 460  
TGCCCATCTGGATCACAGCCAGAGGCAGGGCCTGAGGGCTGGCTCCTTCTTCTACCCGGGCGGGAACGTCACCTACC  
P I W I T A Q R Q G L R A G S F F Y P G G N V T Y Q  
470 480 490 500 510 520 530 540  
AAGGGGTGGCTGTGACGCGGAGCCGGAAGAAGGCATCGCACACAACCTACAAAAATGAGACGGAGTGGAGAGCGAACA  
G V A V T R S R K E G I A H N Y K N E T E W R A N I  
550 560 570 580 590 600 610 620  
TCGACACAGTGTGGCTGGTTCACAGAGGAGGACCTGGATCTGGTCACACTCTACTTCGGGGAGCCGGACTCCACGG  
D T V M A W F T E E D L D L V T L Y F G E P D S T G  
630 640 650 660 670 680 690 700  
GCCACAGGTACGGCCCCGAGTCCCCGAGAGGAGGAGATGGTGCAGGTGGACCGGACCGTGGGCTACCTCCGGG  
H R Y G P E S P E R R E M V R Q V D R T V G Y L R E  
710 720 730 740 750 760 770 780  
AGAGCATCGCGCAACACCTCACAGACCGCTCAACCTGATCATCATCCGACCACGGCATGACGACCGTGGACA  
S I A R N H L T D R L N L I I T S D H G M T T V D K

Figure 3a

790 800 810 820 830 840 850  
AACGGGCTGGCGACCTGGTTGAATTCACAAGTTCCCAACTTCACCTTCGGGACATCGAGTTTGAGCTCCTGGACT  
R A G D L V E F H K F P N F T F R D I E F E L L D Y

860 870 880 890 900 910 920 930  
ACGGACCAACGGGATGCTGCTCCCTAAAGAAGGGAGGCTGGAGAAGGTGTACGATGCCCTCAAGGACGCCACCCCA  
G P N G M L L P K E G R L E K V Y D A L K D A H P K

940 950 960 970 980 990 1000 1010  
AGCTCCACGTCTACAAGAAGGAGGCGTTCCCCGAGGCCTTCCACTACGCCAACAACCCAGGGTCACACCCCTGCTGA  
L H V Y K K E A F P E A F H Y A N N P R V T P L L M

1020 1030 1040 1050 1060 1070 1080 1090  
TGACAGCGACCTTGGCTACGTCATCCATGGGAGAATTAACGTCCAGTTCAACAATGGGGAGCACGGCTTTGACAA  
Y S D L G Y V I H G R I N V Q F N N G E H G F D N K

1100 1110 1120 1130 1140 1150 1160 1170  
AGGACATGGACATGAAGACCATCTCCGCGCTGTGGGCCCTAGCTTCAGGGCGGGCCTGGAGGTGGAGCCCTTTGAGA  
D M D M K T I F R A V G P S F R A G L E V E P F E S

1180 1190 1200 1210 1220 1230 1240  
GCGTCCACGTGTACGAGCTCATGTGCCGGCTGCTGGGCATCGTGCCGAGGCCAACGATGGGCACCTAGCTACTCTGC  
V H V Y E L M C R L L G I V P E A N D G H L A T L L

1250 1260 1270 1280 1290 1300 1310 1320  
TGCCCATGCTGCACACAGAATCTGCTCTTCGCGCTGATGCTCTGCTGGTCGCGGACGGACCCTGCCTCCCCAGCTTAT  
P M L H T E S A L P P D A L L V A D G P C L P S L S

1330 1340 1350 1360 1370 1380 1390 1400  
CCCAGGCCAGAGGCTGCATGCCACTGTCCCGGCAGCGCCCAACCCCTGCTTGGCTGTTATGGTGCTGGTAATAAGCCT  
Q A R G C M P L S P A A P T P A W L L W C W

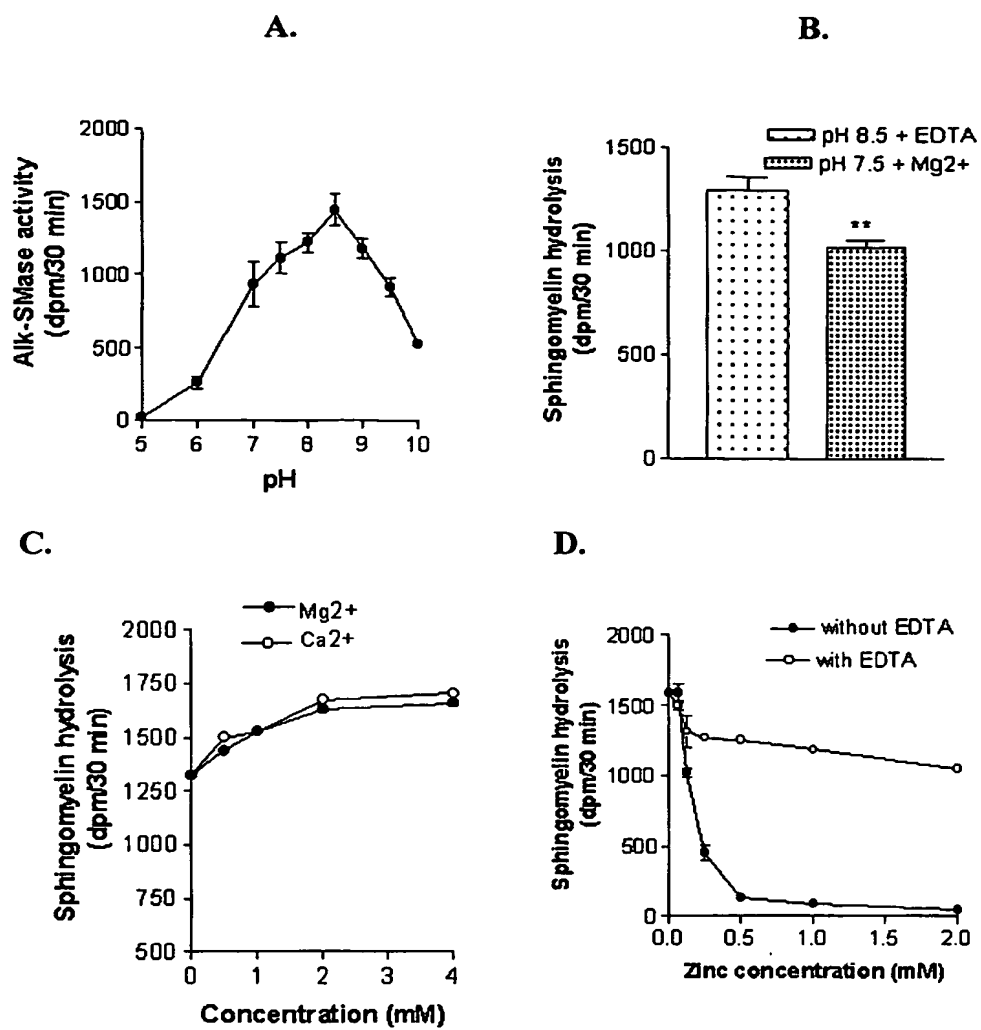
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TTCGGGCCCCCTCCTCTGCAAAACCCGCTCCCGAAGCGGCGCTGCCGTCTGCAGCCACGCGGGGGCGCGGGGAGTC

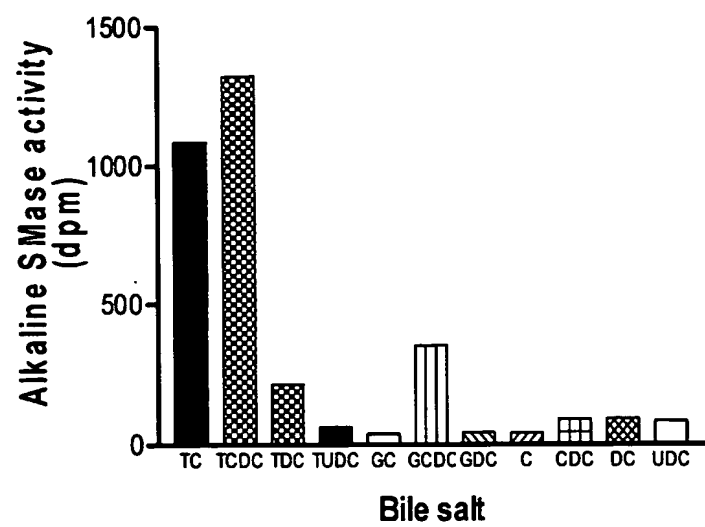
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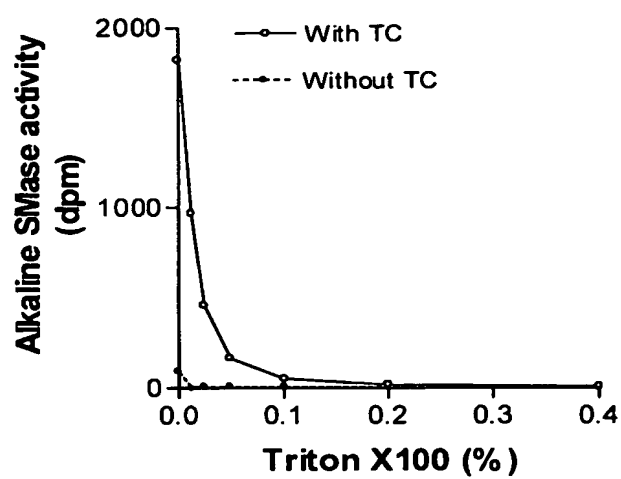
1570 1580 1590 1600 1610 1620 1630  
TTCTGCGGGCGCTGGAACCTGCAGACCCGGCCTCGGTCTGCTGAGGGGGCCCCGCGGCAAAAGCACCCATGGGA

1640 1650 1660 1670 1680 1690 1700  
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Figure 3b

**Figure 4**

**Figure 5**

**Figure 6**

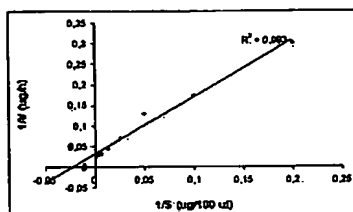
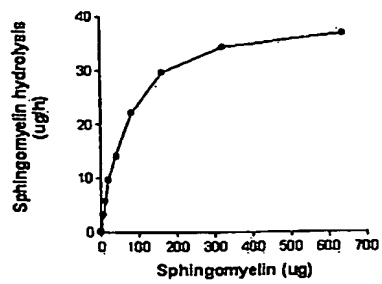


Figure 7



CTATTTAGGT	GACACTATAG	AACAAGTTTG	TACAAAAAAG	CAGGCTGGTA
CCGGTCCGGA	ATTCCCGGGA	TGTCCATCTG	GAAGGCCAG	CATGAGAGGC
CCGGCCGTCC	TCCTCACTGT	GGCTCTGGCC	ACGCTCCTGG	CTCCCGGGGC
CGGAGCACCG	GTACAAAGTC	AGGGCTCCCA	GAACAAGCTG	CTCCTGGTGT
CCTTCGACGG	CTTCCGCTGG	AACTACGACC	AGGACGTGGA	CACCCCCAAC
CTGGACGCCA	TGGCCCGAGA	CGGGGTGAAG	GCACGCTACA	TGACCCCCGC
CTTTGTCACC	ATGACCAGCC	CCTGCCACTT	CACCCTGGTC	ACCGGCAAAT
ATATCGAGAA	CCACGGGGTG	GTTCAACA	TGTACTACAA	CACCACCAGC
AAGGTGAAGC	TGCCCTACCA	CGCCACGCTG	GGCATCCAGA	GGTGGTGGGA
CAACGGCAGC	GTGCCCATCT	GGATCACAGC	CCAGAGGCAG	GGCCTGAGGG
CTGGCTCCTT	CTTCTACCCG	GGCGGGAACG	TCACCTACCA	AGGGGTGGCT
GTGACGCGGA	GCCGGAAGA	AGGCATCGCA	CACAACCTACA	AAAATGAGAC
GGAGTGGAGA	GCGAACATCG	ACACAGTGAT	GGCGTGGTTC	ACAGAGGAGG
ACCTGGATCT	GGTCACACTC	TACTTCGGGG	AGCCGGACTC	CACGGGCCAC
AGGTACGGCC	CCGAGTCCCC	GGAGAGGAGG	GAGATGGTGC	GGCAGGTGGA
CCGGACCGTG	GGCTACCTCC	GGGAGAGCAT	CGCGCGCAAC	CACCTCACAG
ACCGCCTCAA	CCTGATCATC	ACATCCGACC	ACGGCATGAC	GACCGTGGAC
AAACGGGCTG	GCGACCTGGT	TGAATTCCAC	AAGTTCCCCA	ACTTCACCTT
CCGGGACATC	GAGTTTGAGC	TCCTGGACTA	CGGACCAAAC	GGGATGCTGC
TCCCTAAAGA	AGGGAGGCTG	GAGAAGGTGT	ACGATGCCCT	CAAGGACGCC
CACCCCAAGC	TCCACGTCTA	CAAGAAGGAG	GCGTTCCCCG	AGGCCTTCCA
CTACGCCAAC	AACCCAGGG	TCACACCCCT	GCTGATGTAC	AGCGACCTTG
GCTACGTCAT	CCATGGGAGA	ATTAACGTCC	AGTTCAACAA	TGGGGAGCAC
GGCTTTGACA	ACAAGGACAT	GGACATGAAG	ACCATCTTCC	GCGCTGTGGG
CCCTAGCTTC	AGGGCGGGCC	TGGAGGTGGA	GCCCTTTGAG	AGCGTCCACG
TGTACGAGCT	CATGTGCCGG	CTGCTGGGCA	TCGTGCCCGA	GGCCAACGAT
GGGCACCTAG	CTACTCTGCT	GCCCATGCTG	CACACAGAAT	CTGCTCTTCC
GCCTGATGCT	CTGCTGGTCTG	CGGACGGACC	CTGCCTCCCC	AGCTTATCCC
AGGCCAAAGG	CTGCATGCCA	CTGTCCCCGG	CAGCGCCAAC	CCCTGCTTGG
CTGTTATGGT	GCTGGTAATA	AGCCTGCAGC	CCAGGTCCAA	AGCCCCCGGC
GAGCCGGTCC	CATAACCGGC	CCCCTGCCCC	TGCCCCCTGCT	CCTGCTCCTC
CCCTTCGGGC	CCCCTCCTCC	TGCAAAAACCC	GCTCCCCAAG	CGGCGCTGCC
GTCTGCAGCC	ACGCGGGGGC	GCGCGGGAGT	CTTCTGCGGG	CGCTGGAACC
TGCAGACCCG	GCCTCGGTCA	GCTGGGAGGG	GCCCCCCCCG	GCACAAAGCA
CCCATGGGAA	TAAAGGCCAA	GCCGCGACAG	TCAGCAAAAA	AAAAAAAAAA
AAAAAAAAAA	AAAAAAAAAA	AGGGCGGCCG	CTCTAGAGTA	TCCCTCGAGG
GGCCCAAGCT	TACGCGTACC	CAGCTTCTT	GTACAAAGTG	GTCCCTATAG
TGAGTCGTAT	TATAAGCTAG	GCA		

Figure 8

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```

Alk-SMase      -----MRGPAVLLTVALATLLAPGAGAPVQSQGSONKLLLVSFEGFRWNYDQD--VDT 51
NPP1_HUMAN     KGDCCTINYSSVCQGEKSWVEEPCESINEPQCAGFETPPTLLFSLGFRAEYLHTWGGLL 232
NPP2_HUMAN     RGDCCTNYQVVCKGESHVDDCEEIKAAECAGFVRPLIIFSVGFRASVMKKGSKVM 186
NPP3_HUMAN     KKCCADYKSVCOGETSWLENCDTAQSCQCEGFDLPVILFSGGFRAEYLYTWDITLM 181
NPP4_HUMAN     -----MKLLVILFSGLITGFRSDSSSLPP-----KLLLVSFEGFRADYLKN--YEF 46
NPP5_HUMAN     -----MTSKFLLVSFILAAALSSTTFSLOPD---QKVLVLSFEGFRWDYLYK--VPT 48
               * * * * *

Alk-SMase      PNLDAMARDGVKARYMTPAFVTMTSPCHFLLVTGKYIENHGTVHNMYYNTTSKVKLPHYA 111
NPP1_HUMAN     PVISKLKCGTGTKNMRPVYPTKTFPNHYSIVTGLYPESHGII DNKMYDPKMNASFSLKS 292
NPP2_HUMAN     PNIEKLKSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRG 246
NPP3_HUMAN     PNINKLKTCGIHSHKMYRAMYPTKTFPNHYTIVTGLYPESHGII DNMYDVNLNKNFSLSS 241
NPP4_HUMAN     PHLQNFIEGVLVEHVKNVITKTFPNHYSIVTGLYEEHSHGIVANSMDAVTKKHFS--D 104
NPP5_HUMAN     PHFHYIMKYGVHVQVNTNVFITKTFPNHYTIVTGLFAENHGIVANDMFDPIRNKSFSLDH 108
               * * * * *

Alk-SMase      TLGIQRWWDNGSVPIWITAQR-QGLRAGSFYPPGGNVITYQGVAVTRSRKEGIAHNYKNET 170
NPP1_HUMAN     KEKFNPEWYKGE-PIWVTAKY-QGLKSGTFFWPGSDVEINGIFPDIYKMYNGSVPFEE- 349
NPP2_HUMAN     REKFNHRWVGGO-PLWITATK-QGVKAGTFFWS-----VVI PHERR- 285
NPP3_HUMAN     KEQNPAPWVHGO-PMWLTAMY-QGLKAATYFWPGSEVAINGSFPSIYMPYNGSVPFEE- 298
NPP4_HUMAN     SNKDPFVWNEAVPIWVTNQLQENRSSAAAMWPGTDVPIHDTISSYFMNYNSVSVFEE- 163
NPP5_HUMAN     MNIYDSKFWEATPIWITNQR-AGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDR- 166
               * * *

Alk-SMase      EWRANIDTVMAWFTEDLDLVTLYFGFEGSTGFRYGP-ESPERREMVRQVDRTVGYLRES 229
NPP1_HUMAN     --ILAVLQWLQLPKDERPHFYTYLLEPPSSGFSYGP-VSSEVIKALQVDMVGMMLMDG 406
NPP2_HUMAN     --ILTILQWLTLDPHERPSVAFYSEQPFSGFKYGP-FGPEMTNPLREIDKIVGQMLMDG 342
NPP3_HUMAN     --ISTLLKWLDPKAERPRFYTYMFEEDSSGFRAGGP-VSARVIKALQVVDHAFGLMMEG 355
NPP4_HUMAN     --LNNITMWNLN-SNPPVTFTATLYWEEPDASGRKYGPEDKENMSRVLKKIDDLIGDLVQR 220
NPP5_HUMAN     --VAKIIEWFT--SKEPINLGLLYWEDPDMDGHLGP-DSPLMGPVISDIDKKLGYLIQM 221
               * * * * *

Alk-SMase      IARNHLTDRLNLIITSDEGMTVTDKRGADLVEFHKFPNFTFRDIEFELLDYGPNGMLLP- 288
NPP1_HUMAN     LKELNLHRCNLNLIISDEGMEQGSCKK-----YIYLNKYLGDVKNIKVIYGAARLRPS 460
NPP2_HUMAN     LKQKLHRCVNVIVFGPHGMEDEVTCDR-----TEFLSNYLTNVDDITLVPGTLGRIR-- 394
NPP3_HUMAN     LKQRLNHCNVNILLADPHGMDQTYCNK-----MEYMTDYFPRINFFYMYEGPAPRIAH 409
NPP4_HUMAN     LKMLGLWENLNVITSDHGMTQCSQDR-----LINLDSCIDHSYTYLIDLSPVAAILP- 273
NPP5_HUMAN     LKKAKLWNTLNLITSDHGMTQCSQDR-----LIELDQYLDKDHYTELIDQSPVAAILP- 274
               * * * * *

Alk-SMase      -----KEGRLEKVYDALKDAHP--KLHVYKKEAFPEAFHYANNPRVTPLLMYSDLYGYVI 340
NPP1_HUMAN     DVDPKYYSFNYEGIANRLSCREPNQHFHPYLPKHLFPAKSDRIEPLTFYLDPOWQL 520
NPP2_HUMAN     SKFSNNAKYDPKAI IANLTCKKPDQHFHPYLPKHLFPAKSDRIEPLTFYLDPOWQL 454
NPP3_HUMAN     NIPHDFFSEIEIVNLSCKRPDQHFHPYLPKHLFPAKSDRIEPLTFYLDPOWQL 469
NPP4_HUMAN     -----KINR-TEVYNKLNKNCSP--HMNVYLKEDI PNRFYYQHNDRIQPIILVADEGWTI 324
NPP5_HUMAN     -----KEGKFDEVYEALTHAHP--NLTVYKKEDEVPERWHYKYSRIQPII IAVADEGWHI 326
               * * * * *

Alk-SMase      HGR-----INVQFNNGEFGFDNKMDMKTI FRAVGPSFRAGLEVEPFESVHVYELMC 392
NPP1_HUMAN     ALN-----PSEKRYCGSGFGSDNVFSNMQALFVGYPGFGKHGIEADTFENIEVYNLMC 574
NPP2_HUMAN     ARKPLDVYKKPSGKCFEFGDFGFDNKVNSMQTVFVGYPGFKYKTKVPFFENIELYNVMC 514
NPP3_HUMAN     VRS-----KSN-TNCGGNGHGYNNEFRSMEAI FLAHGSPFKEKTEVEPFENIEVYNLMC 522
NPP4_HUMAN     VLN-----ESS-QKLGDEGYDNLSPSMHPFLAAGPAFHKGKYSTINIVDIYPMCM 375
NPP5_HUMAN     LQN-----KSDDFLLGNHGYDNALADMHPI FLAHGPAFRKNFSKAMNSTDLYPLLC 378
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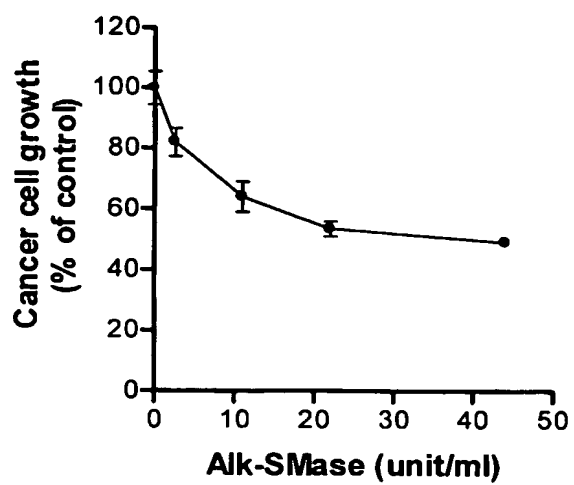
Alk-SMase      RLLGIVPEANDGHLATLLPMLHT----- 415
NPP1_HUMAN     DLLNLTAPANNNGTHGSLNHLKPNVYTPKHPEVHPLVQCPEFR-NPRDNLGCSCN--PS 631
NPP2_HUMAN     DLLGLKAPANNNGTHGSLNHLKPNVYTPKHPEVHPLVQCPEFR-NPRDNLGCSCN--PS 571
NPP3_HUMAN     DLLRIQAPANNNGTHGSLNHLKVPFYEPHAEVSKFSVCGFANPLPTESLDCFCPHLQN 582
NPP4_HUMAN     HILGLKPHPNNGTFGHTKCLL-----VDQWCINLP----- 405
NPP5_HUMAN     HLLNITAMPNNGSFWNVQDLLNSAMPRVVPYTQSTILLPG----- 418
               * * *

Alk-SMase      -----ESALPPDALLVADGPC 431
NPP1_HUMAN     ILPIEDFQTQFNLTVAEEKI IKHETLPYGRPRVLQKENTICLLSQHQFMSGYSQDILMPL 691
NPP2_HUMAN     KVEPKNKLDELNKLRLHTKGSTEERHLLYGRPAVLYR-TRYDILYHTDFESGYSEIFLMPL 630
NPP3_HUMAN     STQLEQVQNMLNLTQEEITATVKVNLFPGRPRVLQKNVDHCLLYHREYVSGFGKAMRMFM 642
NPP4_HUMAN     -----EAI AIVIGSLVLVLTMLTCLIIIM 428
NPP5_HUMAN     -----SVKPAEYDQEGSYPYFVIGSLGSIIVIVFVFIF 451

Alk-SMase      LPSLSQAKGCMPLSPAAPTFAWLLWCW----- 458
NPP1_HUMAN     WTSYTVDRNDSFS--TEDFSNCLYQDFRIPLSPVHKCSFYKNNTKVSYGFLSPPQLNKN 749
NPP2_HUMAN     WTSYTVSKQAEVSSVPDHLTSCVRPDVRSFSPSQNCLAYKNDKQMSYGFLEPPYLSSSP 690
NPP3_HUMAN     WSSYTVPQLGOTSPLPPTVPDCLRADVRVPPSESQKCSFYLADKNITHGFLYPPASNRTS 702
NPP4_HUMAN     QNRLSVPRPFSRLQLQEDDDDLIG----- 453
NPP5_HUMAN     IKHLIHSQIPALQDMHAEIAQPLLOA----- 477

```

Figure 9

**Figure 10**

MRGPAVLLTV ALATLLAPGA GAPVQSQGSQ NKLLLVSF DG FRWNYDQDVD TPNLDAMARD 60  
GVKARYMTPA FVTMTSPCHF TLVTGKYIEN HGVVHNMYYN TTSKVKLPHY ATLG IQRWWD 120  
NGSVPIWITA QRQGLRAGSF FYPGGNVTYQ GVAVTRSRKE GIAHNYKNET EWRANIDTVM 180  
AWFTEEDLDL VTLYFGEPDS TGHRYGPESP ERREMVRQVD RTVGYLRESI ARNHLTDRLN 240  
LIITSDHGMT TVDKRAGDLV EFHKFPNFTF RDIEFELLDY GPNGMLLPKE GRLEKVDYDAL 300  
KDAHPKLHVV KKEAFPEAFH YANNPRVTPL LMYS DLGYVI HGRINVQFNN GEHGFDNKDM 360  
DMKTIFRAVG PSFRAGLEVE PFESVHVYEL MCRL LGIVPE ANDGHLATLL PMLHTESALP 420  
PDGRPTLLPK GRSALPPSSR PLLVMG LLGT VILLSEVA 458

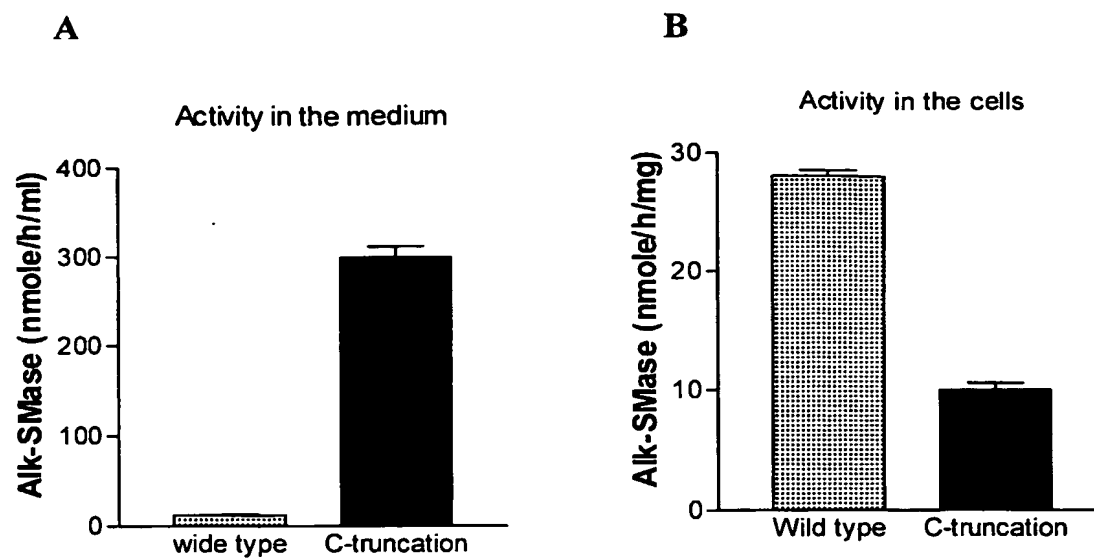
**Figure 11**

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GCTCTGGCCA CGCTCCTGGC TCCCGGGGCC GGAGCACCGG TACAAAGTCA 100
GGGCTCCCAAG AACAAGCTGC TCCTGGTGTC CTTCGACGGC TTCCGCTGGA 150
ACTACGACCA GGACGTGGAC ACCCCCAACC TGGACGCCAT GGCCCGAGAC 200
GGGGTGAAGG CACGCTACAT GACCCCCGCC TTTGTCACCA TGACCAGCCC 250
CTGCCACTTC ACCCTGGTCA CCGGCAAATA TATCGAGAAC CACGGGGTGG 300
TTCACAACAT GTACTACAAC ACCACCAGCA AGGTGAAGCT GCCCTACCAC 350
GCCACGCTGG GCATCCAGAG GTGGTGGGAC AACGGCAGCG TGCCCATCTG 400
GATCACAGCC CAGAGGCAGG GCCTGAGGGC TGGCTCCTTC TTCTACCCGG 450
GCGGGAACGT CACCTACCAA GGGGTGGCTG TGACGCGGAG CCGGAAAGAA 500
GGCATCGCAC ACAACTACAA AAATGAGACG GAGTGGAGAG CGAACATCGA 550
CACAGTGATG GCGTGGTTCA CAGAGGAGGA CCTGGATCTG GTCACACTCT 600
ACTTCGGGGA GCCGGACTCC ACGGGCCACA GGTACGGCCC CGAGTCCCCG 650
GAGAGGAGGG AGATGGTGCG GCAGGTGGAC CGGACCGTGG GCTACCTCCG 700
GGAGAGCATC GCGCGCAACC ACCTCACAGA CCGCCTCAAC CTGATCATCA 750
CATCCGACCA CGGCATGACG ACCGTGGACA AACGGGCTGG CGACCTGGTT 800
GAATTCCACA AGTTCCCCAA CTTACCTTC CGGGACATCG AGTTTGAGCT 850
CCTGGACTAC GGACCAAACG GGATGCTGCT CCCTAAAGAA GGGAGGCTGG 900
AGAAnGTGTA CGATGCCCTC AAGGACGCCC ACCCCAAGCT CCACGTCTAC 950
AAGAAGGAGG CGTTCCCCGA GGCCTTCCAC TACGCCAACA ACCCCAGGGT 1000
CACACCCCTG CTGATGTACA GCGACCTTGG CTACGTCATC CATGGGAGAA 1050
TTAACGTCCA GTTCAACAAT GGGGAGCACG GCTTTGACAA CAAGGACATG 1100
GACATGAAGA CCATCTTCCG CGCTGTGGGC CCTAGCTTCA GGGCGGGCCT 1150
GGAGGTGGAG CCCTTTGAGA GCGTCCACGT GTACGAGCTC ATGTGCCGGC 1200
TGCTGGGCAT CGTGCCCGAG GCCAACGATG GGCACCTAGC TACTCTGCTG 1250
CCCATGCTGC ACACAGAATC TGCTCTTCCG CCTGATGGAA GGCCTACTCT 1300
CCTGCCCCAAG GGAAGATCTG CTCTCCCGCC CAGCAGCAGG CCCCTCCTCG 1350
TGATGGGACT GCTGGGGACC GTGATTCTTC TGTCTGAGGT CGCATAACGC 1400
CCCATGGCTC AAGGAAGCCG CCGGGAGCTG CCCGCAGGCC CTGGGCCGGC 1450
TGTCTCGCTG CGATGCTCTG CTGGTCGCGG ACGGACCCTG CCTCCCCAGC 1500
TTATCCCAGG CCAGAGGCTG CATGCCACTG TCCCCGGCAG CGCCAACCCC 1550
TGCTTGCTG TTATGGTGCT GGTAATAAGC CTCGCAGCCC AGGTCCAGAG 1600
CCCCCGGCGA GCCGGTCCCA TAACCGGCCC CCTGCCCCTG CCCCTGCTCC 1650
TGCTCCTCCC CTTCGGGCCC CCTCCTCCTG CAAAACCCGC TCCCGAAGCG 1700
GCGCTGCCGT CTGCAGCCAC GCGGGGGCGC GCGGGAGCTC TGCGGGCGCT 1750
GGAACCTGCA GACCCGGCCT CGGTCAGCTG GGAGGGGCCC GCCCCGGCAC 1800
AAAGCACCCA TGGAATAAAA GGCCAAGCCG CGACAGTCAG CAAAAAAAAA 1841
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Figure 12

**Figure 13**